

Figure 1

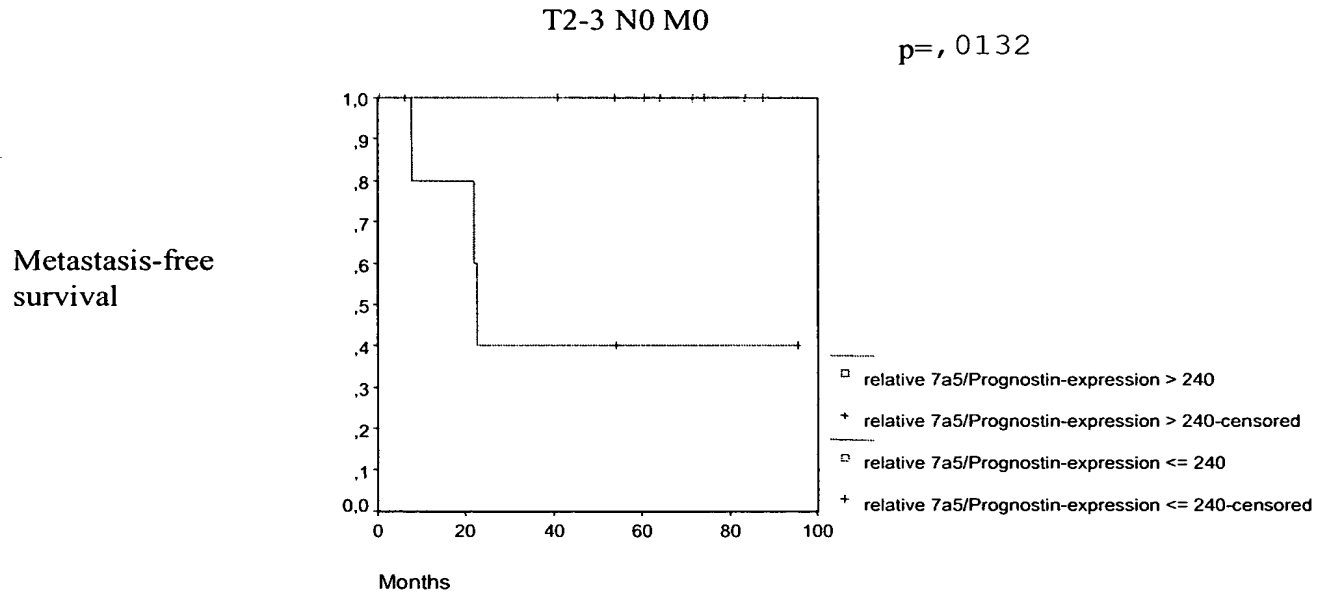


Figure 2

relative 7a5/Prognostin-
expression

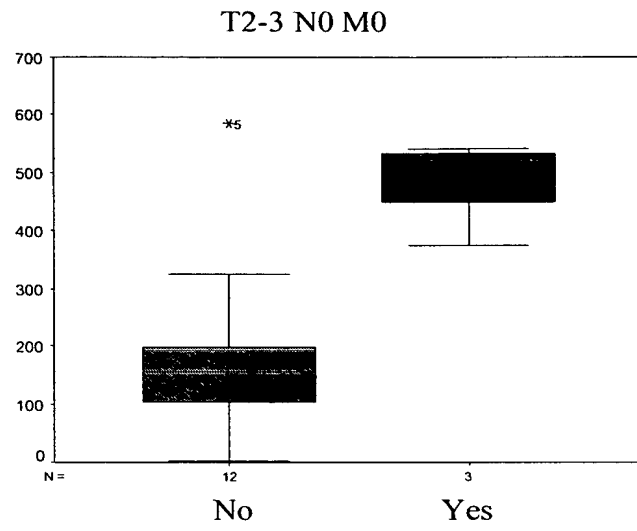


Figure 3

1 ATGCTAATCACTGAAAGAAAAACATTTTCGGTCAGGAAGAATTGCACAAAGTATGTCTGAAGCAAATTTGATTGACATGGAAGCTGGAAGAACTCTCAAAAAGTTGCAATATTACAGAATGC
M L I T E R K H F R S G R I A Q S M S E A N L I D M E A G K L S K S C N I T E C

121 CAGGACCCAGACTTGCTTCACAATTGGCCGGATGCTTTCACCCCTTCGTGGTAATAATGCTTCCAAAGTTGCAATCCATTCTGGAATCAACTGTCTGCTTCTAACCCATTTTGGATGAC
Q D P D L L H N W P D A F T L R G N N A S K V A N P F W N Q L S A S N P F L D D

241 ATAACCACTAAGAATAACAGGAAGAGAAATAATATTCCATCTTAAAGGAAGATCCTTTCTTTCTGTAGAGAAATAGAAAATGGAATTTCTTTGATTCTCCGGTGATGAACCTT
I T Q L R N N R K R N N I S I L K E D P F L F C R E I E N G N S F D S S G D E L

361 GATGTGCATCAGTTACTTAGGCAGACTTCTCAAGAAATTCGGAAGATCTAAAGTGTTCGAACTTCTGGACATTTTAGACGACACAGCACATGCCATCAGAGTATACATACTCT
D V H Q L L R Q T S S R N S G R S K S V S E L L D I L D D T A H A H Q S I H N S

481 GACCAGATCCTACTACAGACTTAGAGTGGCTTAAAAATGATCGGGAGGCTTATAAAATGGCTTGGTTAAGTCAACGCCAGCTGGCCCGCTCCTGCCTTGATTGAAATACAATTAGTCAG
D Q I L L H D L E W L K N D R E A Y K M A W L S Q R Q L A R S C L D L N T I S Q

601 AGCCCTGGATGGGCCCAGACACAACCTTGGGAGGTCACCATAGCTTGAAGTAAACCATCAAGGAGGTCAGTACAATTACCTGAATCAGACATCACTGTTCTAGTGCCCCAAGGTCAT
S P G W A Q T Q L A E V T I A C K V N H Q G G S V Q L P E S D I T V H V P Q G H

721 GTGGCTGTGGGAGAATCCAAAGAGGTGTCTCTAAGGGCTTCTTGTATCCGCCACATGCTTAACCATGATCTTTCGTGCACTGTGAGCCCGCTTGTGGAAATCATGTTAGGCAACCTC
V A V G E F Q E V S L R A F L D P P H M L N H D L S C T V S P L L E I M L G N L

841 AATACAATGAAGCCCTTTTGTGGAGATGAAAATTTGGGCTGAAGTAAAGAGGATCCTTTCAGCAAGTCATGACAGAAATGGTGTGTATACAGCTTGGGTAAAGAGGCCCTTTT
N T M E A L L L E M K I G A E V R K D P F S Q V M T E M V C L H S L G K E G P F

961 AAAGTTTTAAGCACTGCTACATTTATAAAGACACCATCAAGTCAAGCTAATCGACTTGAGTCAGGTAATGTATCTAGTGGTGTGTCACAAGCTAAAGCTCTCCGTCACAGCTGCC
K V L S N C Y I Y K D T I Q V K L I D L S Q V M Y L V V A A Q A K A L P S P A A

1081 ACCATTTGGGATTATATCCACAAAACACCTCAATTGGAATTTATGGAGCCAAATATATCCATCCAGTTTACTGTTGTTTTAACAGTTTGTGGACACAATTATATGCCAGGACAGCTT
T I W D Y I H K T T S I G I Y G P K Y I H P S F T V V L T V C G H A N Y P G G Q L

1201 ACAATTTCTGATATTAAAGAGGTTGAAAAACATATCTCCAGTTGTGTTTCAGCTCTGGGGGAAGCAGTCATTTTACTTGACAAGCCACAAGATTAAAGTATTCTATTTTTCTCTGT
T I S D I K K G G K N I S P V V F Q L W G K Q S F L L D K P Q D L S I S I F S C

1321 GATCCTGATTTTGAAGTAAAGACAGAGGAGAAAGGAAAGAAATTAACAAAAGCAGTTGGAAGCAGGTGAAGTAGTTTCATCAACAATTTTTATTTTCTTTAGTTGAGCAGAGAGATG
D P D F E V K T E G E R K E I K Q K Q L E A G E V V H Q Q F L F S L V E H R E M

1441 CACTTGTGTGATTTTGTGTTCAAGTGGAGCCTCCCAATGGTGAACAGTTGCACAGTTCTCTATCACTACTCTGATCAACCCCAACCTTAAAGAGCTCTCGAATCTGCCAGGCTAT
H L F D F C V Q V E P P N G E P V A Q F S I T T P D P T P N L K R L S N L P G Y

1561 TTGCAGAAGAAGGAGGAAATCAAGTCTGCTCTCTTATCACCAAAAATTTCTGTTAAATATCTACATTTCAAGATAAAACATTGAACTTTAGCAACTATGGGTAACCTCAAGGCAGTG
L Q K K E E I K S A P L S P K I L V K Y P T F Q D K T L N F S N Y G V T L K A V

1681 CTAAGACAAAGCAAGATTGATTACTTCTTTGAATATTCAAAAGGGACACAATAGCTCTCTCGGGGAAGGTAAGGTAAAGCTATTGGTCAGTCCAAAGTGAAAGAAATGGTATGTAGGA
L R Q S K I D Y F L E Y F K G D T I A L L G E G K V K A I G Q S K V K E W Y V G

1801 GTCTCTCAGAGTAAAGATTGCACTTGTACACTGCAAAAATGTCAGCTGATTTCAAAGGAGCAAGTAATGTTATGTCAGATAGTGTCTTTACAACAGAAATCTTTGAACAGATTGTC
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1921 CTGCCCTTTAAAAAATGACTTATATCTACTCAGTTGTATTAACTTGGTGTGAGAAAAGTTTATGATTGCAAGTTTACCTGATGCTCTGCTGATCACAATCTGCTCCCTGGAAGAT
L P L K K L T Y I Y S V V L T L V S E K V Y D W K V L A D V L G Y S H L S L E D

2041 TTTGATCAAATTCAGCAGACAAAGAAATCAGAGAAAGTTCTTATGTTATAAAGAAAGTTAAAGGAAGATTGCCACACAGAGAGAAATACAAGGAAGTTTCTGTATGAACCTATTGTGGCT
F D Q I Q A D K E S E K V S Y V I K K L K E D C H T E R N T R K F L Y E L I V A

2161 CTTCTGAAAATGGATTGCAAGAGTTAGTCGCACGTCTCATCCAAGAGCTGCTGTTCTGACTTCAGCTGTCAAGCTTGGAAAAGGCTGGAGGGAAGTACTGCTGAAAAGTTAGTACGACTC
L L K M D C Q E L V A R L I Q E A A V L T S A V K L G K G W R E L A E K L V R L

2281 ACAAGCAACAAATGGAGGCATATGAAATTCCTCATCGAGGAAACACTGGAGATGTTGCTGTTGAGATGATGTGGAAGCTGCTTATGATTCTGCTGATACCTGGAGTGCTCACTATGGA
T K Q Q M E A Y E I P H R G N T G D V A V E M M W K P A Y D F L Y T W S A H Y G

2401 AATAACTACAGAGATGTGTTACAAGACCTTCAGTCAGCTTTGGAGAGAATGAAAACCTGTGACTAAACACTGGAGAGAATTAACCTGGAGTTTAACTAGTAAATCTTTGGAGGTT
N N Y R D V L Q D L Q S A L D R M K N P V T K H W R E L T G V L I L V N S L E V

2521 TTGAGAGTAACCTGCACTTCTCCACTTCTGAGGAAGTATAG
L R V T A F S T S E E V *

Figure 4

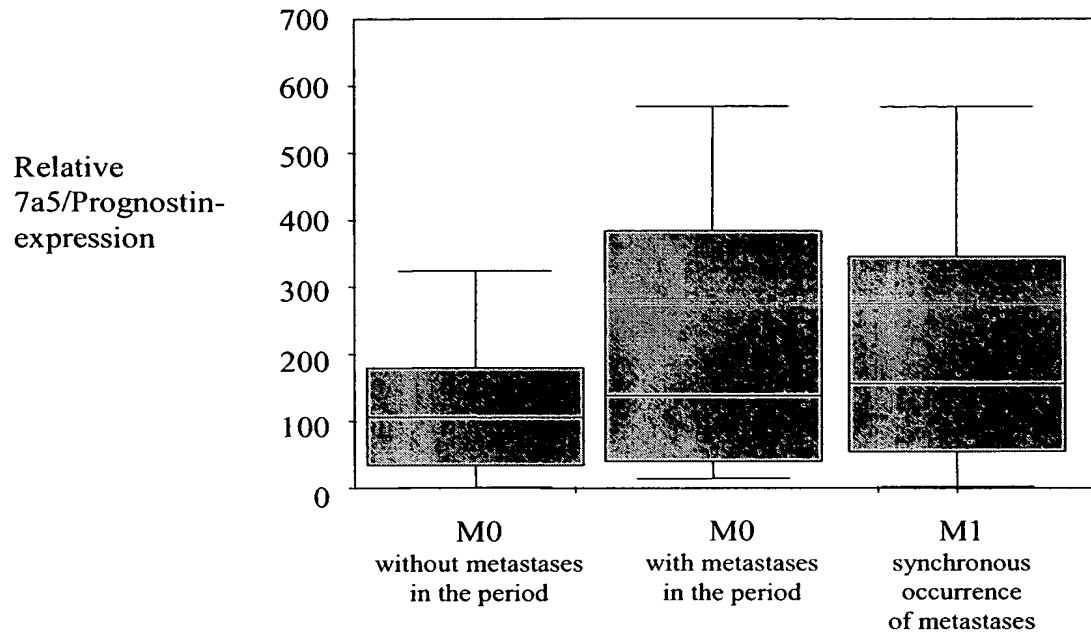


Figure 5

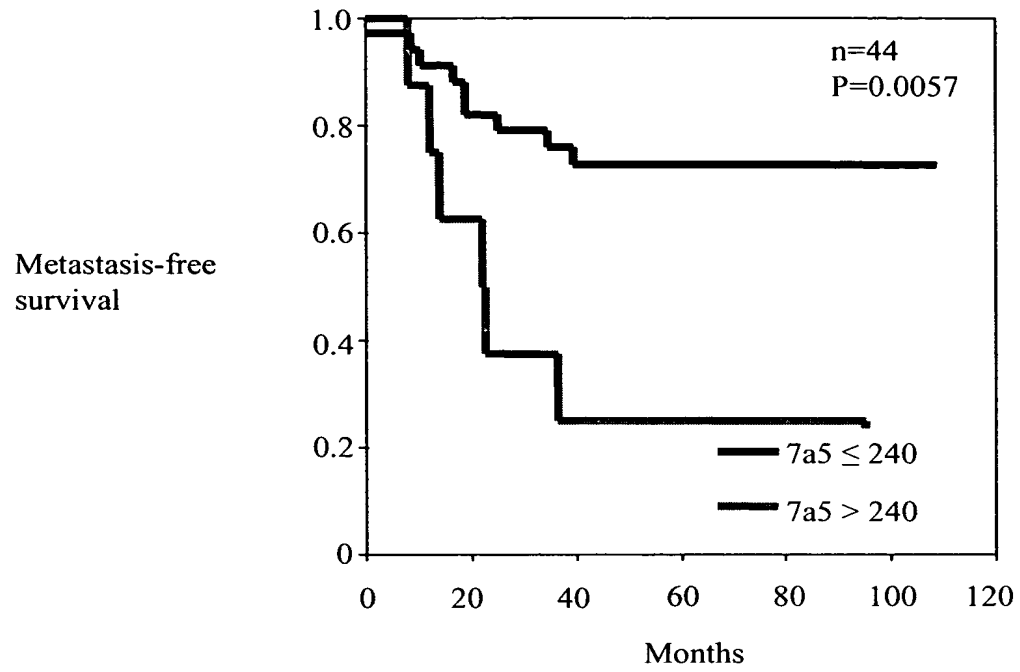
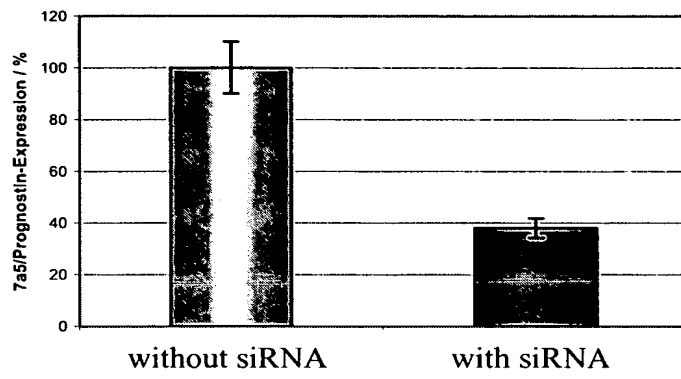


Figure 6

A



B

